

STIC-Biot ch/ChemLib

93410

From: Schultz, James
Sent: Wednesday, May 07, 2003 9:22 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 10/057,550

RECEIVED

MAY - 7 2003

TECH/CHEM. DIVISION
(STIC)

Whoops, sorry, the corrected file name is now listed in the title above.

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Wednesday, May 07, 2003 9:06 AM
To: Schultz, James
Subject: RE: Sequence search pct/us02/04123

This Application Number does not have a valid CRF - please provide the necessary correction or another application number.

maude

-----Original Message-----

From: Schultz, James
Sent: Wednesday, May 07, 2003 8:36 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search pct/us02/04123

Hello,

I need a length limited nucleotide sequence search performed on SEQ ID NO: 64 in the above entitled application, where the maximum size of the returned hit is no more than 50 nucleotides long. Thanks,
Doug Schultz

J. Douglas Schultz, Ph.D.
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 5/18/03
Date Completed: 5/17/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: ADN
Sequence Sys.: 01
WWW/Internet: _____
Other (specify): _____



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk



GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 05:03:09 ; Search time 7722 Seconds

(without alignments)
11219.769 Million cell updates/sec

Title: US-10-057-550a-64

Perfect score: 2977

Sequence: 1 ccgaatgaccgcctcccg.....taataataataaattt 2977

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
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- 8: gb_pl:*
- 9: gb_pr:*
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- 13: gb_un:*
- 14: gb_vl:*
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- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
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- 23: em_pat:*
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- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rtd:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	32.8	1.1	49	9	HUMRAF12	L00213 Human c-raf
2	30.6	1.0	31	6	AX248756	AX248756 Sequence
3	28	0.9	28	6	AR090859	AR090859 Sequence
4	28	0.9	28	6	AR197894	AR197894 Sequence
5	26	0.9	26	6	AR090860	AR090860 Sequence
6	26	0.9	26	6	AR197895	AR197895 Sequence
7	26	0.9	26	6	196168	196168 Sequence 5
8	26	0.9	26	6	196169	196169 Sequence 6
9	25	0.8	25	6	AR110776	AR110776 Sequence
10	22.2	0.7	50	6	AX157157	AX157157 Sequence
11	22	0.7	43	6	AR079693	AR079693 Sequence
12	22	0.7	43	6	AR081223	AR081223 Sequence
13	22	0.7	43	6	AR142002	AR142002 Sequence
14	22	0.7	43	6	AR170583	AR170583 Sequence
15	22	0.7	50	6	AX164948	AX164948 Sequence
16	21.6	0.7	50	6	AX159540	AX159540 Sequence
17	21.4	0.7	40	6	AR100922	AR100922 Sequence
18	21.4	0.7	40	6	AR100937	AR100937 Sequence
19	21.2	0.7	35	6	A63574	A63574 Sequence 15
20	21.2	0.7	44	9	HUMMACG	L37694 Homo sapien
21	21	0.7	31	6	AX119347	AX119347 Sequence
22	21	0.7	40	6	AR100923	AR100923 Sequence
23	21	0.7	40	6	AR100938	AR100938 Sequence
24	20.8	0.7	27	6	A63567	A63567 Sequence 8
25	20.6	0.7	21	6	AX096685	AX096685 Sequence
26	20.6	0.7	36	6	AX119579	AX119579 Sequence
27	20.6	0.7	50	6	AX159538	AX159538 Sequence
28	20.4	0.7	27	6	A63562	A63562 Sequence 3
29	20.4	0.7	27	6	A63571	A63571 Sequence 12
30	20.4	0.7	27	6	A63572	A63572 Sequence 13
31	20.4	0.7	30	6	AR208293	AR208293 Sequence
32	20.4	0.7	33	6	AR027238	AR027238 Sequence
33	20.4	0.7	40	6	AX147000	AX147000 Sequence
34	20.4	0.7	50	6	AX426994	AX426994 Sequence
35	20.2	0.7	33	6	AX253351	AX253351 Sequence
36	20.2	0.7	33	6	AX253358	AX253358 Sequence
37	20.2	0.7	38	6	AX183838	AX183838 Sequence
38	20.2	0.7	45	9	HUMNEF28	L27066 Human neuro
39	20.2	0.7	46	6	AX287576	AX287576 Sequence
40	20.2	0.7	46	6	AX287580	AX287580 Sequence
41	20.2	0.7	48	6	AX277277	AX277277 Sequence
42	20.2	0.7	48	6	I58003	I58003 Sequence 11
43	20	0.7	20	6	A52104	A52104 Sequence 7
44	20	0.7	20	6	A52105	A52105 Sequence 8
45	20	0.7	20	6	A52132	A52132 Sequence 5

ALIGNMENTS

RESULT 1
LOCUS HUMRAF12 49 bp DNA linear PRI 08-JAN-1995
DEFINITION Human c-raf-1 proto-oncogene, exon 2, clones lambda-(2.13).
ACCESSION L00213
VERSION L00213.1 GI:190830
KEYWORDS c-myc proto-oncogene; raf protein; raf proto-oncogene.
SEGMENT 2 of 9
SOURCE Homo sapiens (tissue library: of Lawn et'al.) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Bonner,T.I., Kerby,S.B., Sutcliffe,P., Gunnell,M.A., Mark,G. and
Rapp,U.R.

TITLE structure and biological activity of human homologs of the raf/ml oncogene
JOURNAL Mol. Cell. Biol. 5 (6), 1400-1407 (1985)
MEDLINE 85295973
PubMed 2993863
COMMENT See comment in segment 1.
FEATURES Location/Qualifiers
SOURCE 1..49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="3p25"
/tissue_lib="Of Lawn et al."
/tissue_lib="Of Lawn et al."
1..15
/gene="RAF1"
/note="G00-119-546"
/number=1
16..43
/gene="RAF1"
/note="G00-119-546"
/number=2
44..>49
/gene="RAF1"
/note="G00-119-546"
/number=2
Intron
BASE COUNT 12 a 11 c 10 g 16 t
ORIGIN About 3.7 kb after segment 1; chromosome 3p25.
Query Match 1.1%; Score 32.8; DB 9; Length 49;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 956 TGATTGAGATGCAATTCGAGTCACAGCAGATCAG 991
DB 8 TGTTTCAGATGCAATTCGAGTCACAGCAGATCAG 43
RESULT 2
LOCUS AX248756 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 835 from Patent WO0166800.
ACCESSION AX248756
VERSION AX248756.1 GI:15863379
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 835 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
SOURCE 1..31
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 7 a 9 c 5 g 9 t 1 others
ORIGIN
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Best Local Similarity 96.8%; Pred. No. 4.8e+03;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2144 CCCTTCTCCAGAGCAGAACACATGTTTC 2174
DB 1 CCCTTCTCCAGAGCAGAACACATGTTTC 31
RESULT 3
LOCUS AR090859 28 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 979 from patent US 5994076.
ORIGIN

ACCESSION AR090859
VERSION AR090859.1 GI:10017614
KEYWORDS
MEDLINE
PubMed
COMMENT
FEATURES Location/Qualifiers
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik, A., Johhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 979 30-NOV-1999;
FEATURES Location/Qualifiers
SOURCE 1..28
/organism="unknown"
BASE COUNT 5 a 8 c 5 g 10 t
ORIGIN
Query Match 0.9%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1704 CAGTTCCAGTCGATGCTACTCTAT 1731
DB 1 CAGTTCCAGTCGATGCTACTCTAT 28
RESULT 4
LOCUS AR197894 28 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 979 from patent US 6352829.
ACCESSION AR197894
VERSION AR197894.1 GI:20247743
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik, A., Johhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 979 05-MAR-2002;
FEATURES Location/Qualifiers
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BASE COUNT 5 a 8 c 5 g 10 t
ORIGIN
Query Match 0.9%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1704 CAGTTCCAGTCGATGCTACTCTAT 1731
DB 1 CAGTTCCAGTCGATGCTACTCTAT 28
RESULT 5
LOCUS AR090860/c 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 980 from patent US 5994076.
ACCESSION AR090860
VERSION AR090860.1 GI:10017615
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik, A., Johhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 980 30-NOV-1999;
FEATURES Location/Qualifiers
SOURCE 1..26
/organism="unknown"
BASE COUNT 4 a 6 c 9 g 7 t
ORIGIN

Query Match 0.9%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1963 TCTCTACCGAAGATCAACCGGACCGC 1988
|||||
DB 26 TCTCTACCGAAGATCAACCGGACCGC 1

RESULT 6
ARI97895/c ARI97895 26 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 980 from patent US 6352829.
DEFINITION ARI97895
ACCESSION ARI97895
VERSION ARI97895.1 GI:20247744
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik, A., Johhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 980 05-MAR-2002;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 4 a 6 c 9 g 7 t

Query Match 0.9%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1963 TCTCTACCGAAGATCAACCGGACCGC 1988
|||||
DB 26 TCTCTACCGAAGATCAACCGGACCGC 1

RESULT 7
196168/c 196168 26 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 5 from patent US 5734039.
DEFINITION 196168
ACCESSION 196168
VERSION 196168.1 GI:3940638
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Calabretta, B. and Skorski, T.
TITLE Antisense oligonucleotides targeting cooperating oncogenes
JOURNAL Patent: US 5734039-A 5 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 5 a 4 c 14 g 3 t

Query Match 0.9%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATGTGACCGCTCCGCTCCCTCACC 30
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DB 26 ATGTGACCGCTCCGCTCCCTCACC 1

RESULT 8
196169 196169 26 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 6 from patent US 5734039.
DEFINITION 196169
ACCESSION 196169

VERSION 196169.1 GI:3940639
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Calabretta, B. and Skorski, T.
TITLE Antisense oligonucleotides targeting cooperating oncogenes
JOURNAL Patent: US 5734039-A 6 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 3 a 14 c 4 g 5 t

Query Match 0.9%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATGTGACCGCTCCGCTCCCTCACC 30
|||||
DB 1 ATGTGACCGCTCCGCTCCCTCACC 26

RESULT 9
ARI10776/c ARI10776 25 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 2 from patent US 6126965.
DEFINITION ARI10776
ACCESSION ARI10776
VERSION ARI10776.1 GI:12827624
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kasid, U., Gokhale, P., Ditschilo, A. and Rahman, A.
TITLE Liposomes containing oligonucleotides
JOURNAL Patent: US 6126965-A 2 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..25
BASE COUNT 4 a 7 c 6 g 8 t

Query Match 0.8%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GCTGCATCATGAGACATACAG 145
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DB 25 GCTGCATCATGAGACATACAG 1

RESULT 10
AX157157/c AX157157 50 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 485 from Patent W00140521.
DEFINITION AX157157
ACCESSION AX157157
VERSION AX157157.1 GI:14538488
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R. A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 485 07-JUN-2001;
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"

misc_feature /db_xref="taxon:9606"
25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg44928329"
misc_feature 26
/note="1 of 2 allelic variants (486 is other entry)"
BASE COUNT 29 a 8 c 7 g 6 t
ORIGIN

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Best Local Similarity 77.1%; Pred. No. 1.3e+06;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2875 TTCTGATGATTTGGGTTTATTTGTTTATT 2909
DB 50 TTCTCAGATGATTTGGGTTTATTTGTTTATT 16

RESULT 11
LOCUS AR079693 43 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 17 from patent US 5965726.
ACCESSION AR079693
VERSION AR079693.1 GI:10006434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Pavlakis,G.N. and Felber,B.K.
TITLE Method of eliminating inhibitory/instability regions of mRNA
JOURNAL Patent: US 5965726-A 17 12-OCT-1999;
FEATURES
source 1..43
/organism="unknown"

BASE COUNT 9 a 11 c 5 g 18 t
ORIGIN

Query Match 0.7%; Score 22; DB 6; Length 43;
Best Local Similarity 73.7%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 2207 TCACAGGGCCTTAACCTGATGCTTCCTTTCTATC 2244
DB 2 TCTCAGATACCTAGCTTCATATGCTTATGCTTACC 39

RESULT 12
LOCUS AR081223 43 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 17 from patent US 5972596.
ACCESSION AR081223
VERSION AR081223.1 GI:10007949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Pavlakis,G.N. and Felber,B.K.
TITLE Nucleic acid constructs containing HIV genes with mutated inhibitory/instability regions and methods of using same
JOURNAL Patent: US 5972596-A 17 26-OCT-1999;
FEATURES
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/organism="unknown"

BASE COUNT 9 a 11 c 5 g 18 t
ORIGIN

Query Match 0.7%; Score 22; DB 6; Length 43;
Best Local Similarity 73.7%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 2207 TCACAGGGCCTTAACCTGATGCTTCCTTTCTATC 2244

DB 2 TCTCAGATACCTAGCTTCATATGCTTATGCTTACC 39

RESULT 13
LOCUS AR142002 43 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 17 from patent US 6174666.
ACCESSION AR142002
VERSION AR142002.1 GI:15102302
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Pavlakis,G.N. and Felber,B.K.
TITLE Method of eliminating inhibitory/instability regions from mRNA
JOURNAL Patent: US 6174666-A 17 16-JAN-2001;
FEATURES
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/organism="unknown"

BASE COUNT 9 a 11 c 5 g 18 t
ORIGIN

Query Match 0.7%; Score 22; DB 6; Length 43;
Best Local Similarity 73.7%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 2207 TCACAGGGCCTTAACCTGATGCTTCCTTTCTATC 2244
DB 2 TCTCAGATACCTAGCTTCATATGCTTATGCTTACC 39

RESULT 14
LOCUS AR170583 43 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6291664.
ACCESSION AR170583
VERSION AR170583.1 GI:17908542
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Pavlakis,G.N. and Felber,B.K.
TITLE Method of eliminating inhibitory/instability regions of mRNA
JOURNAL Patent: US 6291664-A 17 18-SEP-2001;
FEATURES
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/organism="unknown"

BASE COUNT 9 a 11 c 5 g 18 t
ORIGIN

Query Match 0.7%; Score 22; DB 6; Length 43;
Best Local Similarity 73.7%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 2207 TCACAGGGCCTTAACCTGATGCTTCCTTTCTATC 2244
DB 2 TCTCAGATACCTAGCTTCATATGCTTATGCTTACC 39

RESULT 15
LOCUS AX164948 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 143 from Patent W00138586.
ACCESSION AX164948
VERSION AX164948.1 GI:14545777
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 50)
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 143 31-MAY-2001;
Curagen Corporation (US)

FEATURES
source 1. .50
Location/Qualifiers

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/organism="Homo sapiens".
/db_xref="taxon:9606"

variation
26
/note="Nucleotide deleted between bases 25 and 26
Accession number c943945210"

BASE COUNT 9 a 11 c 8 g 22 t
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Best Local Similarity 83.3%; Pred. No. 1.5e+06;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2804 AAACAACAACAACGCTTCTCTCT 2833
DB 33 AAACAACAACAACAACGCTTCTCTCT 4

Search completed: May 16, 2003, 09:18:22
Job time : 7741 secs

GenCore version 5.1.4_p5_4578
(c) 1993 - 2003 CompuGen Ltd.

cleic search, using sw model

May 16, 2003, 05:00:24 ; Search time 629 Seconds

10658.504 million cell updates/sec

Title: US-10-057-550A-64
Pagefoot: 2077

Sequence: 1 ccgaatgtgaccgcctccg.....tataaataaacttaattt 2977

Scoring table: IDENTITY_NUC
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

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Minimum DB seq length: 0
Maximum DB seq length: 50
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
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Listing first 45 summaries

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11:	/SID2/gcgdata/genseq/genseqn-emb1/NA1991.DAT *
12:	/SID2/gcgdata/genseq/genseqn-emb1/NA1992.DAT *
13:	/SID2/gcgdata/genseq/genseqn-emb1/NA1993.DAT *
14:	/SID2/gcgdata/genseq/genseqn-emb1/NA1994.DAT *
15:	/SID2/gcgdata/genseq/genseqn-emb1/NA1995.DAT *
16:	/SID2/gcgdata/genseq/genseqn-emb1/NA1996.DAT *
17:	/SID2/gcgdata/genseq/genseqn-emb1/NA1997.DAT *
18:	/SID2/gcgdata/genseq/genseqn-emb1/NA1998.DAT *
19:	/SID2/gcgdata/genseq/genseqn-emb1/NA1999.DAT *
20:	/SID2/gcgdata/genseq/genseqn-emb1/NA2000.DAT *
21:	/SID2/gcgdata/genseq/genseqn-emb1/NA2001A.DAT *
22:	/SID2/gcgdata/genseq/genseqn-emb1/NA2001B.DAT *
23:	/SID2/gcgdata/genseq/genseqn-emb1/NA2002.DAT *
24:	/SID2/gcgdata/genseq/genseqn-emb1/NA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35.6	1.2	42	21	AAA07016	Raf-1 mutagenic P
2	32.6	1.1	39	21	AAA07027	Raf-1 mutagenic P
3	32.4	1.1	42	21	AAA07017	Raf-1 mutagenic P
4	31	1.0	31	22	AAI130347	Human single nucle
5	28	0.9	28	24	ABK66891	Human gene specific
6	26	0.9	26	19	AAV20480	Human c-raf antisense
7	26	0.9	26	24	ABK66892	Human gene specific
8	25	0.9	50	22	AAI133396	Human SNP Oligonucle
9	25	0.8	25	22	AAH44455	Human latexin prot

C	10	24.2	0.8	35	21	AAA29996	Haifpin hybridizer
C	11	24	0.8	24	19	AAV33096	C-raf probe 5' Sy
C	12	24	0.8	31	21	AAA30000	Haifpin hybridizer
C	13	24	0.8	33	21	AAA29998	Haifpin hybridizer
C	14	23	0.8	23	21	AAA26239	C-raf antisense ol
C	15	23	0.8	23	21	AAA26242	C-raf antisense ol
C	16	23	0.8	23	21	AAA26243	C-raf antisense ol
C	17	23	0.8	23	21	AAA26244	C-raf antisense ol
C	18	23	0.8	23	21	AAA26245	C-raf antisense ol
C	19	23	0.8	23	21	AAA26246	C-raf antisense ol
C	20	22.4	0.8	27	22	AAH41610	Human c-Raf1 PCR p
C	21	22.4	0.8	27	24	ABL50197	Human c-Raf1 PCR p
C	22	22.4	0.8	27	24	ABL50229	Human c-Raf1 PCR p
C	23	22.4	0.8	50	22	AA131673	Human SNP oligonuc
C	24	22.2	0.7	27	18	AA193884	Phosphodiester oli
C	25	22.2	0.7	50	22	AA173544	Human silent SNP c
C	26	22	0.7	30	22	AAH41550	Human c-Raf1 PCR p
C	27	22	0.7	30	24	ABL50177	Human c-Raf1 PCR p
C	28	22	0.7	30	24	ABL50209	Human c-Raf1 PCR p
C	29	22	0.7	41	18	AA193841	Phosphodiester oli
C	30	22	0.7	43	14	AA050213	c-fos position 339
C	31	22	0.7	47	21	AA269529	Human map-related
C	32	22	0.7	50	23	ABL00152	Human silent nonco
C	33	21.6	0.7	50	22	AA175927	Human silent SNP c
C	34	21.4	0.7	40	19	AAV05430	Human RAS5f5 use
C	35	21.4	0.7	40	19	AAV05418	Primer used in pro
C	36	21.4	0.7	40	21	AAAT2878	Yeast Rf gene PCR
C	37	21.4	0.7	40	21	AAAT2893	Yeast PCR primer R
C	38	21.4	0.7	40	21	AAAS5851	RAF PCR primer SEQ
C	39	21.4	0.7	40	21	AAAS5866	GAD plasmid RAS in
C	40	21.2	0.7	35	18	AAAT3823	Antitumoural phosph
C	41	21	0.7	21	22	AAAF97088	Human gene single
C	42	21	0.7	27	22	AAHA1589	Human c-Raf1 PCR p
C	43	21	0.7	27	24	ABL50176	Human c-Raf1 PCR p
C	44	21	0.7	27	24	ABL50208	Human c-Raf1 PCR p
C	45	21	0.7	40	19	AAV05431	Primer RAS5f4 use

ALIGNMENTS

RESULT 1
AAA07016
ID AAA07016 standard; DNA; 42 BP.
AC AAA07016;
XX
DT 03-JUL-2000 (first entry)
XX
DE Raf-1 mutagenic PCR primer, SEQ ID NO:13.
XX
KX Raf-1; GTP kinase; phosphorylation; ceramide-activated protein kinase
KW mutagenesis; lipopolysaccharide; LPS; endotoxin;
KW sphingomyelin signal transduction pathway; PCR primer; ss.
XX
XX Mammalia.
OS Synthetic.
XX
PN US6040149-A.
XX
PD 21-MAR-2000.
XX
PF 10-JAN-1997; 97US-0785247.
XX
XX 11-JAN-1996; 96US-0009900.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Zhang Y, Liu J, Kolesnick RN;
XX
DR WPI; 2000-270133/23.
XX
XT Novel method of identifying agents capable of inhibiting

PT lipopolysaccharide induced threonine phosphorylation by a
PT ceramide-activated protein kinase
XX
XX
PS Example VI; Column 56; 84pp; English.
XX
CC The invention relates to a novel method of determining whether an agent
CC is capable of specifically inhibiting the ability of a
CC ceramide-activated protein (CAP) kinase to phosphorylate the threonine
CC residue in a polypeptide containing a Thr-Pro- or Thr-Leu-Pro motif. In
CC particular, the peptide substrate that is specifically phosphorylated is
CC Raft-1, epidermal growth factor receptor (EGFR), or suitable fragments
CC thereof. The CAP kinase is membrane bound and has an apparent molecular
CC weight of 100-110 kD. It is an upstream participant in a sphingomyelin
CC signal transduction pathway which uses ceramide as a second messenger.
CC This pathway is initiated by tumour necrosis factor- α (TNF- α)
CC and interleukin-beta (IL-beta), causing the hydrolysis of sphingomyelin
CC to ceramide. The ceramide in turn stimulates the kinase to
CC phosphorylate protein substrates which can then mediate signal
CC transduction. The CAP kinase is also stimulated by the bacterial
CC endotoxin lipopolysaccharide (LPS), which is thought to mimic the second
CC messenger function of ceramide. The methods are useful for identifying
CC agents that inhibit lipopolysaccharide-induced Thr phosphorylation by
CC CAP kinase. The agents identified using the method are useful for
CC treating disorders associated with aberrant phosphorylation of target
CC molecules by CAP kinase, e.g., inflammatory disorders (such as rheumatoid
CC arthritis), ulcerative colitis, graft versus host disease, lupus
CC erythematosus, HIV, infection, disorders associated with poor stem cell
CC growth, and septic shock. Sequences AAA07016-A07019 and AAA07027
CC represent PCR primers used in an exemplification of the present invention
CC to generate mutant Flag peptide/Raft-1 sequences via overlap extension
CC PCR.
XX
SQ Sequence 42 BP; 9 A; 12 C; 14 G; 7 T; 0 other;
XX
Query Match 1.2%; Score 35.6; DB 21; Length 42;
Best Local Similarity 90.5%; Pred. No. 1.4;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 916 GTCCACATGTCACGACGCGTCTGTCGACGACGATG 957
Db 1 GTCCACATGTCACGCGTACCGGTGACACGACGATG 42
XX
RESULT 2
ID AAA07027 standard; DNA: 39 BP.
XX
AC AAA07027;
XX
DT 03-JUL-2000 (first entry)
XX
DE Raft-1 mutagenic PCR primer, SEQ ID NO:27;
XX
KW Raft-1; CAP kinase; phosphorylation; ceramide-activated protein kinase;
KW mutagenesis; lipopolysaccharide; LPS; endotoxin;
KW sphingomyelin signal transduction pathway; PCR primer; ss.
XX
OS Mammalia.
OS Synthetic.
XX
PN US6040149-A.
XX
PD 21-MAR-2000.
XX
PF 10-JAN-1997; 97US-0785247.
XX
PR 11-JAN-1996; 96US-0009900.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX Zhang Y, Liu J, Kolesnick RN;
XX
PI WPI; 2000-270133/23.

XX
PT Novel method of identifying agents capable of inhibiting
PT lipopolysaccharide induced threonine phosphorylation by a
PT ceramide-activated protein kinase
XX
XX
PS Example VI; Column 56; 84pp; English.
XX
CC The invention relates to a novel method of determining whether an agent
CC is capable of specifically inhibiting the ability of a
CC ceramide-activated protein (CAP) kinase to phosphorylate the threonine
CC residue in a polypeptide containing a Thr-Pro- or Thr-Leu-Pro motif. In
CC particular, the peptide substrate that is specifically phosphorylated is
CC Raft-1, epidermal growth factor receptor (EGFR), or suitable fragments
CC thereof. The CAP kinase is membrane bound and has an apparent molecular
CC weight of 100-110 kD. It is an upstream participant in a sphingomyelin
CC signal transduction pathway which uses ceramide as a second messenger.
CC This pathway is initiated by tumour necrosis factor- α (TNF- α)
CC and interleukin-beta (IL-beta), causing the hydrolysis of sphingomyelin
CC to ceramide. The ceramide in turn stimulates the kinase to
CC phosphorylate protein substrates which can then mediate signal
CC transduction. The CAP kinase is also stimulated by the bacterial
CC endotoxin lipopolysaccharide (LPS), which is thought to mimic the second
CC messenger function of ceramide. The methods are useful for identifying
CC agents that inhibit lipopolysaccharide-induced Thr phosphorylation by
CC CAP kinase. The agents identified using the method are useful for
CC treating disorders associated with aberrant phosphorylation of target
CC molecules by CAP kinase, e.g., inflammatory disorders (such as rheumatoid
CC arthritis), ulcerative colitis, graft versus host disease, lupus
CC erythematosus, HIV, infection, disorders associated with poor stem cell
CC growth, and septic shock. Sequences AAA07016-A07019 and AAA07027
CC represent PCR primers used in an exemplification of the present invention
CC to generate mutant Flag peptide/Raft-1 sequences via overlap extension
CC PCR.
XX
SQ Sequence 39 BP; 9 A; 11 C; 13 G; 6 T; 0 other;
XX
Query Match 1.1%; Score 32.6; DB 21; Length 39;
Best Local Similarity 89.7%; Pred. No. 1.1;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 919 CACATGTCACGACGCGTCTGTCGACGACGATG 957
Db 1 CACATGTCACGACGCGTCTACCGTGTGACGACGATG 39
XX
RESULT 3
ID AAA07017 standard; DNA: 42 BP.
XX
AC AAA07017;
XX
DT 03-JUL-2000 (first entry)
XX
DE Raft-1 mutagenic PCR primer, SEQ ID NO:14.
XX
KW Raft-1; CAP kinase; phosphorylation; ceramide-activated protein kinase;
KW mutagenesis; lipopolysaccharide; LPS; endotoxin;
KW sphingomyelin signal transduction pathway; PCR primer; ss.
XX
OS Mammalia.
OS Synthetic.
XX
PN US6040149-A.
XX
PD 21-MAR-2000.
XX
PF 10-JAN-1997; 97US-0785247.
XX
PR 11-JAN-1996; 96US-0009900.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX Zhang Y, Liu J, Kolesnick RN;
XX
PI

XX
DR WPI: 2000-270133/23.
XX
PT Novel method of identifying agents capable of inhibiting
PT lipopolysaccharide induced threonine phosphorylation by a
PT ceramide-activated protein kinase
XX
PS Example VI: Column 56, 84pp: English.
XX
CC The invention relates to a novel method of determining whether an agent
CC is capable of specifically inhibiting the ability of a
CC ceramide-activated protein (CAP) kinase to phosphorylate the threonine
CC residue in a polypeptide containing a Thr-Pro or Thr-Leu-Pro motif. In
CC particular, the peptide substrate that is specifically phosphorylated is
CC Raf-1, epidermal growth factor receptor (EGFR), or suitable fragments
CC thereof. The CAP kinase is membrane bound and has an apparent molecular
CC weight of 100-110 kD. It is an upstream participant in a sphingomyelin
CC signal transduction pathway which uses ceramide as a second messenger.
CC This pathway is initiated by tumour necrosis factor-alpha (TNF-alpha)
CC and interleukin-beta (IL-beta), causing the hydrolysis of sphingomyelin
CC to ceramide. The ceramide in turn stimulates the kinase to
CC phosphorylate protein substrates which can then mediate signal
CC transduction. The CAP kinase is also stimulated by the bacterial
CC endotoxin lipopolysaccharide (LPS), which is thought to mimic the second
CC messenger function of ceramide. The methods are useful for identifying
CC agents that inhibit lipopolysaccharide-induced Thr phosphorylation by
CC CAP kinase. The agents identified using the method are useful for
CC treating disorders associated with aberrant phosphorylation of target
CC molecules by CAP kinase, e.g., inflammatory disorders (such as rheumatoid
CC arthritis), ulcerative colitis, graft versus host disease, lupus
CC erythematosus, HIV, infection, disorders associated with poor stem cell
CC growth, and septic shock. Sequences AAA07016-A07019 and AAA07027
CC represent PCR primers used in an exemplification of the present invention
CC to generate mutant flag peptide/Raf-1 sequences via overlap extension
CC PCR.
XX
SQ Sequence 42 BP: 8 A; 11 C; 15 G; 8 T; 0 other;
XX
Query Match 1.1%; Score 32.4; DB 21; Length 42;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 916 GTCCACATGTCGACACGACGTCCTGTGACAGCAGATG 957
DB 1 GTCCACATGTCGACGTCGTGACGTCGTCGACAGCAGATG 42
XX
RESULT 4
AAI30347
ID AAI30347 standard; DNA; 31 BP.
XX
AC AAI30347;
XX
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) RAF1.
XX
KM Human; resequence; genotype; disease; forensic; paternity testing;
KM single nucleotide polymorphism; SNP; ss.
XX
XX Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
FT Variation replace(16,T)
FT /tag a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200166800-A2.
XX
XX 13-SEP-2001.
XX
XX 07-MAR-2001; 2001WO-US07268.
XX

PR 07-MAR-2000; 2000US-0187510.
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI: 2001-522952/57.
XX
XX Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype
XX
XX Claim 1; Page 80; 145pp: English.
XX
XX The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
SQ Sequence 31 BP: 7 A; 10 C; 5 G; 9 T; 0 other;
XX
Query Match 1.0%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2144 CCTTCTCCAGAGCAGACACATGTTTC 2174
DB 1 CCTTCTCCAGAGCAGACACATGTTTC 31
XX
RESULT 5
ABK66891
ID ABK66891 standard; DNA; 28 BP.
XX
AC ABK66891;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human gene specific PCR primer #979.
XX
XX Primer; ss; DNA microarray; differential expression analysis; human.
XX
KM Homo sapiens.
XX
OS
XX
PN US6352829-B1.
XX
PD 05-MAR-2002.
XX
PF 05-JAN-1999; 99US-0225928.
XX
PR 21-MAY-1997; 97US-0859998.
XX
XX (CLON-) CLONTECH LAB INC.
XX
PA
PI Chenchik A, Johhadze G, Biblilashvili R;
XX
DR WPI: 2002-314699/35.
XX
XX Producing sub-population of labeled nucleic acids, useful for analysing
PT differences in RNA profiles between several different physiological
PT sources, using set of distinct gene specific primers
XX
XX Example 3; SEQ ID No 979; 11pp; English.
XX
XX The invention relates to producing a sub-population of labeled nucleic
CC acids (NAs) comprising contacting a NA sample from a physiological

CC source, with a pool of 50 distinct gene specific primers under suitable
 CC conditions to enzymatically generate sub-population of NAs, where
 CC each gene specific primer has a sequence complementary to a distinct
 CC mRNA, and each labeled NA is generated using a single gene specific
 CC primer. The method is useful for producing a sub-population of labeled
 CC NAs which is useful for analysing the differences in the RNA profiles
 CC between several different physiological sources, where the method
 CC comprises producing subpopulation of labeled NAs for the different
 CC physiological sources, comprising the populations for each physiological
 CC source to identify differences in the populations, where the comparison
 CC is preferably performed by hybridising the labeled NAs for each of the
 CC distinct physiological sources to an array of probe NAs stably
 CC associated with the surface of a substrate to produce a hybridisation
 CC pattern for each of the sources, and comparing the patterns for each of
 CC the sources, where differential gene expression assays are
 CC utilised in differential expression analysis of diseased a normal
 CC tissue e.g. neoplastic a normal tissue, or different tissue or
 CC subissue types. The present sequence is a human gene specific PCR
 CC primer used in the method of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from USPTO at
 CC http.wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.
 CC
 SQ Sequence 28 BP; 5 A; 8 C; 5 G; 10 T; 0 other;

Query Match 0.9%; Score 28; DB 24; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1704 CAGTTTCAGTCGATGCTACTCTAT 1731
 |||||
 DB 1 CAGTTTCAGTCGATGCTACTCTAT 28

RESULT 6
 AAV20480/c
 ID AAV20480 standard; DNA; 26 BP.

AAV20480;

17-JUN-1998 (first entry)

Human c-raf antisense oligonucleotide.

Human; oncogene; proto-oncogene; neoplastic disease; anticancer;
 cancer; antisense oligonucleotide; phosphorothioate; ss.

Synthetic.
 Homo sapiens.

Key Location/Qualifiers
 FT 1..26
 FT allele /tag= "a
 FT /note= "phosphorothioate linkages"

US5734039-A.

31-MAR-1998.

15-SEP-1994; 94US-0306691.

15-SEP-1994; 94US-0306691.

(UYJE-) UNIV JEFFERSON THOMAS.

Calabretta B, Skorski T;

WPI; 1998-229882/20.

Anticancer composition comprising two anti-sense oligo-nucleotide(s)
 targeting cytoplasmic and nuclear oncogene(s)

PS Example 4; Column 33; 92pp; English.

XX The present sequence represents an antisense oligonucleotide from the
 CC present invention. The present invention describes a composition which
 CC comprises two antisense oligonucleotides. The first oligonucleotide is
 CC specific for a cytoplasmic oncogene or proto-oncogene selected from
 CC ras, raf, EGF-1, c-fms, c-fos, c-kit, c-met, c-trlk, c-src, c-abl,
 CC bcr-abl, c-fgr and c-yes. The second oligonucleotide is specific for a
 CC nuclear oncogene or proto-oncogene selected from myc, jun, c-eis,
 CC c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spl, cyclin D1, PM/RAR
 CC alpha, AML1/MTG8, E2A/P1 and ALU-1/AF-4. The composition is used for
 CC treating cancer. The combination of antisense oligonucleotides has
 CC synergistically enhanced ability to inhibit growth of cancer cells.

SQ Sequence 26 BP; 5 A; 4 C; 14 G; 3 T; 0 other;

Query Match 0.9%; Score 26; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ATGTACCGCCCTCCGCTCCCTACCC 30
 |||||
 DB 26 ATGTACCGCCCTCCGCTCCCTACCC 1

RESULT 7
 ABK66892/c
 ID ABK66892 standard; DNA; 26 BP.

ABK66892;

02-JUL-2002 (first entry)

Human gene specific PCR primer #980.

Primer; ss; DNA microarray; differential expression analysis; human.

Homo sapiens.

US6352829-B1.

05-MAR-2002.

05-JAN-1999; 99US-0225928.

21-MAY-1997; 97US-0859998.

(CLON-) CLONTECH LAB INC.

Chenchik A, Jorhadze G, Biblilashvili R;

WPI; 2002-314699/35.

Producing sub-population of labeled nucleic acids, useful for analysing
 differences in RNA profiles between several different physiological
 sources, using set of distinct gene specific primers

Example 3; SEQ ID No 980; 11pp; English.

The invention relates to producing a sub-population of labeled nucleic
 acids (NAs) comprising contacting a NA sample from a physiological
 source, with a pool of 50 distinct gene specific primers under suitable
 conditions to enzymatically generate sub-population of NAs, where
 each gene specific primer has a sequence complementary to a distinct
 mRNA, and each labeled NA is generated using a single gene specific
 primer. The method is useful for producing a sub-population of labeled
 NAs which is useful for analysing the differences in the RNA profiles
 between several different physiological sources, where the method
 comprises producing subpopulation of labeled NAs for the different
 physiological sources, comprising the populations for each physiological
 source to identify differences in the populations, where the comparison
 is preferably performed by hybridising the labeled NAs for each of the
 distinct physiological sources to an array of probe NAs stably

by them may be used in the prevention, diagnosis and treatment of

2882 7C A T T T C C T T T T T T A A T T T T T C T T T T T T T T 2886

CC the amplified product. The MC-PCR reaction can amplify one or more
CC target mRNAs in a sample using the primer set #1-#5 for each target
CC mRNA. In the example given, primers #1, #2, #3, #4 and probe #5
CC are the C-raf primers 1 (AAV33092), 2 (AAV33093), 3 (AAV33094), 4
CC (AAV33095) and probe 5 respectively. These primers/probes were used to
CC illustrate the method of the invention. The method claims to allow
CC detection of low-abundance mRNA in small samples (e.g. 10 ng is
CC sufficient) with high precision, and uses housekeeping genes as controls
CC for RNA input and integrity. Also, a large number of samples may be
CC processed simultaneously, making the process suitable for high
CC throughput screening, and does not require continuous monitoring.
XX
SQ Sequence 24 BP; 7 A; 9 C; 3 G; 5 T; 0 other;
OY Query Match 0.8%; Score 24; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 GCACAGTATCTACACCTCAGC 24
OY 816 GCACAGTATCTACACCTCAGC 839
|||||
ID AAA30000/c
AA30000 standard; DNA; 31 BP.
XX
AC AAA30000;
XX
DT 09-AUG-2000 (first entry)
XX
DE Hairpin hybridizer molecule #5 targeting c-raf RNA.
XX
KM DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW c-raf; inhibitor; detect; nuclease resistance; gene function;
KM gene expression modulator; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT stem_loop 1..31
FT /*tag- a
FT misc_RNA 1..11
FT /*tag- b
FT /*note- "2'-O-methyl-ribonucleotides"
FT 1..4
FT /*tag- c
FT /*note- "Phosphorothioate internucleotide linkage"
FT 12..20
FT /*tag- d
FT /*note- "Phosphorothioate internucleotide linkage"
FT 21..31
FT /*tag- e
FT /*note- "2'-O-methyl-ribonucleotides"
FT 28..31
FT /*tag- f
FT /*note- "Phosphorothioate internucleotide linkage"
XX
PN WO200017346-A2.
PD 30-MAR-2000.
XX
XX 20-SEP-1999; 99WO-US21865.
PF
XX 21-SEP-1998; 98US-0101174.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX PA
XX PI Hartmann T, Zwick M, Thompson J, Jarvis T;
XX DR WPI; 2000-292841/25.
XX
PT Modulating target sequence in a cell, useful e.g. therapeutically or

PT for identifying gene function, by treatment with novel hairpin
PT hybridizer nucleic acid molecules
XX
PS Claim 3; Page 76; 128pp; English.
XX
XX A method for modulating the function of a target sequence in a cell
CC comprises treatment with a hairpin hybridizer (HPH) nucleic acid molecule
CC such as that represented by the present sequence. The present HPH
CC molecule is used in an example of the invention and targets the human
CC c-raf gene. The HPH molecules function through RNA/DNA inhibition. The
CC HPH molecule binds to and blocks the function of a target nucleic acid,
CC and modulated cellular and viral processes such as splicing, editing, and
CC translation. The HPH molecule can be used therapeutically, in target
CC validation, to identify gene function and/or therapeutic targets, for
CC analysis of mutations in diseased cell and to detect specific RNA. The
CC hairpin structure improves resistance to nuclease degradation,
CC localization within the cell, and uptake by cells. The HPH may include a
CC sequence that activates RNase H (for cleaving RNA) and its specificity is
CC greater than for linear antisense sequences.
XX
SQ Sequence 31 BP; 6 A; 7 C; 11 G; 1 T; 6 U; 0 other;
OY Query Match 0.8%; Score 24; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 27 ATCAATGCTTGACGCTGACCAG 4
OY 2029 ATCAATGCTTGACGCTGACCAG 2052
|||||
ID AAA29998/c
AA29998 standard; DNA; 33 BP.
XX
AC AAA29998;
XX
DT 09-AUG-2000 (first entry)
XX
DE Hairpin hybridizer molecule #3 targeting c-raf RNA.
XX
KM DNA-RNA hybrid; phosphorothioate; hairpin hybridizer molecule; HPH;
KW c-raf; inhibitor; detect; nuclease resistance; gene function;
KM gene expression modulator; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT stem_loop 1..33
FT /*tag- a
FT misc_RNA 1..12
FT /*tag- b
FT /*note- "2'-O-methyl-ribonucleotides"
FT 1..4
FT /*tag- c
FT /*note- "Phosphorothioate internucleotide linkage"
FT 13..21
FT /*tag- d
FT /*note- "Phosphorothioate internucleotide linkage"
FT 22..33
FT /*tag- e
FT /*note- "2'-O-methyl-ribonucleotides"
FT 30..33
FT /*tag- f
FT /*note- "Phosphorothioate internucleotide linkage"
XX
PN WO200017346-A2.
PD 30-MAR-2000.
XX
XX 20-SEP-1999; 99WO-US21865.
PF
XX 21-SEP-1998; 98US-0101174.
XX
PR

XX (RIBO-) RIBOZYME PHARM INC.
PA Hartmann T, Zwick M, Thompson J, Jarvis T;
PI WPI: 2000-292841/25.
XX
XX Modulating target sequence in a cell, useful e.g. therapeutically or
PT for identifying gene function, by treatment with novel hairpin
XX hybridizer nucleic acid molecules
XX
PS Claim 44; Page 76; 128pp; English.
XX
CC A method for modulating the function of a target sequence in a cell
CC comprises treating with a hairpin hybridizer (HPH) nucleic acid molecule
CC such as that represented by the present sequence. The present HPH
CC molecule is used in an example of the invention and targets the human
CC c-ras gene. The HPH molecules function through RNA/DNA inhibition. The
CC HPH molecule binds to and blocks the function of a target nucleic acid,
CC and modulates cellular and viral processes such as splicing, editing, and
CC translation. The HPH molecule can be used therapeutically, in target
CC validation, to identify gene function and/or therapeutic targets, for
CC analysis of mutations in diseased cell and to detect specific RNA. The
CC hairpin structure improves resistance to nuclease degradation,
CC localization within the cell, and uptake by cells. The HPH may include a
CC sequence that activates RNase H (for cleaving RNA) and its specificity is
CC greater than for linear antisense sequences.
XX
SO Sequence 33 BP; 6 A; 8 C; 12 G; 1 T; 6 U; 0 other;
XX
Query Match 0.88; Score 24; DB 21; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2029 ATCAATGCTTGCACGCTGACACG 2052
DB 28 ATCAATGCTTGCACGCTGACACG 5
XX
RESULT 14
AAA26239/c
ID AAA26239 standard; DNA: 23 BP.
XX
AC AAA26239;
XX
DT 19-JUL-2000 (first entry)
XX
DE C-ras antisense oligonucleotide sequence SEQ ID NO:2737.
XX
KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US08547.
XX
PR 20-APR-1998; 98US-0082404.
PR 23-JUN-1998; 98US-0103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, McSwiggen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Matulic-Adamic J;
XX
DR WPI: 2000-013248/01.
XX

PT New nucleic acids that interact, and optionally cleave, target
PT sequences, used to treat cancer
XX
XX Example 8; Page 105; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorothioate
CC link, having endonuclease activity. (A) and more generally any
CC catalytic nucleic acid (A) that modulates expression of the estrogen
CC receptor gene, are used to treat cancer (particularly of breast or
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC estrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent estrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent estrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
CC exemplification of the present invention.
XX
SO Sequence 23 BP; 5 A; 4 C; 8 G; 3 T; 3 U; 0 other;
XX
Query Match 0.88; Score 23; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2029 ATCAATGCTTGCACGCTGACACG 2051
DB 23 ATCAATGCTTGCACGCTGACACG 1
XX
RESULT 15
AAA26242/c
ID AAA26242 standard; DNA: 23 BP.
XX
AC AAA26242;
XX
DT 19-JUL-2000 (first entry)
XX
DE C-ras antisense oligonucleotide sequence SEQ ID NO:2740.
XX
KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US08547.
XX
PR 20-APR-1998; 98US-0082404.
PR 23-JUN-1998; 98US-0103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, McSwiggen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Matulic-Adamic J;
XX
DR WPI: 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target
PT sequences, used to treat cancer

XX Example 8: Page 105; 148bp; English.

PS The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any
CC catalytic nucleic acid (A') that modulates expression of the oestrogen
CC receptor gene, are used to treat cancer (particularly of breast or
CC endometrium), in vivo or by transforming cells ex vivo and implanting
CC treated cells, or for other conditions associated with levels of
CC oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC can also be used to correlate inhibition of gene expression with
CC alterations in phenotype, particularly for identification of therapeutic
CC targets, and as research reagents (for RNA, in the same way that
CC restriction endonucleases are used with DNA). The combination of
CC modifications in (A) improves resistance to nucleases, binding affinity
CC and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC their corresponding target sequences. AAA26219 to AAA26271 represent
CC other ribozyme sequences and antisense oligonucleotides used in the
XX exemplification of the present invention.

SQ Sequence 23 BP; 4 A; 8 C; 5 G; 2 T; 4 U; 0 other;

Query Match

Best Local Similarity 0.8%; Score 23; DB 21; Length 23;
Matches 23; Conservative 0; Pred. No. 6.6e+03;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

OY 2483 GAATGCATCTCACAGCGCGGACT 2505

DB 23 GAATGCATCTCACAGCGCGGACT 1

Search completed: May 16, 2003, 07:08:58
Job time : 644 secs

GenCore version 5.1.4-P5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 06:58:12 ; Search time 106 Seconds
(without alignments)
8612.988 Million cell updates/sec

Title: US-10-057-550A-64

Perfect score: 2977

Sequence: 1 ccgaatgacgcctccg.....taataaataaataattt 2977

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/1na/5B.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35.6	1.2	42	US-08-785-247-13	Sequence 13, Appl
2	32.6	1.1	39	US-08-785-247-31	Sequence 31, Appl
3	32.4	1.1	42	US-08-785-247-14	Sequence 14, Appl
4	28	0.9	28	US-08-859-998-979	Sequence 979, Appl
5	28	0.9	28	US-09-225-928-979	Sequence 979, Appl
6	26	0.9	26	US-08-306-691B-5	Sequence 5, Appl
7	26	0.9	26	US-08-306-691B-6	Sequence 6, Appl
8	26	0.9	26	US-08-859-998-980	Sequence 980, Appl
9	26	0.9	26	US-09-225-928-980	Sequence 980, Appl
10	25	0.8	25	US-08-957-327-2	Sequence 2, Appl
11	25	0.8	25	US-09-482-084-2	Sequence 2, Appl
12	22	0.7	43	US-08-850-048-17	Sequence 17, Appl
13	22	0.7	43	US-08-050-478-17	Sequence 17, Appl
14	22	0.7	43	US-07-858-747B-17	Sequence 17, Appl
15	22	0.7	43	US-09-414-117-17	Sequence 17, Appl
16	22	0.7	43	US-09-678-437-17	Sequence 17, Appl
17	21.4	0.7	40	US-08-874-825-9	Sequence 9, Appl
18	21.4	0.7	40	US-08-874-825-25	Sequence 25, Appl
19	21.4	0.7	40	US-08-663-824-9	Sequence 9, Appl
20	21.4	0.7	40	US-08-663-824-25	Sequence 25, Appl
21	21.4	0.7	40	US-09-231-303-9	Sequence 9, Appl
22	21.4	0.7	40	US-09-231-303-25	Sequence 25, Appl
23	21	0.7	40	US-08-874-825-10	Sequence 10, Appl
24	21	0.7	40	US-08-874-825-26	Sequence 26, Appl
25	21	0.7	40	US-08-663-824-10	Sequence 10, Appl
26	21	0.7	40	US-08-663-824-26	Sequence 26, Appl
27	21	0.7	40	US-09-231-303-10	Sequence 10, Appl

C 28	21	0.7	40	US-09-231-303-26	Sequence 26, Appl
C 29	21	0.7	48	US-09-711-889-3	Sequence 3, Appl
C 30	20.4	0.7	30	US-09-163-507-6	Sequence 6, Appl
C 31	20.4	0.7	33	US-08-580-988A-11	Sequence 11, Appl
C 32	20.2	0.7	47	US-08-951-923-41	Sequence 41, Appl
C 33	20.2	0.7	48	US-08-444-734A-11	Sequence 11, Appl
C 34	20	0.7	20	US-08-250-856A-2	Sequence 2, Appl
C 35	20	0.7	20	US-08-250-856A-3	Sequence 3, Appl
C 36	20	0.7	20	US-08-250-856A-4	Sequence 4, Appl
C 37	20	0.7	20	US-08-250-856A-5	Sequence 5, Appl
C 38	20	0.7	20	US-08-250-856A-6	Sequence 6, Appl
C 39	20	0.7	20	US-08-250-856A-7	Sequence 7, Appl
C 40	20	0.7	20	US-08-250-856A-8	Sequence 8, Appl
C 41	20	0.7	20	US-08-250-856A-9	Sequence 9, Appl
C 42	20	0.7	20	US-08-250-856A-10	Sequence 10, Appl
C 43	20	0.7	20	US-08-250-856A-12	Sequence 12, Appl
C 44	20	0.7	20	US-08-250-856A-13	Sequence 13, Appl
C 45	20	0.7	20	US-08-250-856A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-785-247-13
Sequence 13, Application US/08785247
Patent No. 6040149
GENERAL INFORMATION:
APPLICANT: Kolesnick, Richard N.
APPLICANT: Liu, Jun
TITLE OF INVENTION: ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
TITLE OF INVENTION: CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
TITLE OF INVENTION: SUPPRESSOR OF RAS, AND METHODS OF USING SAID AGENTS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,247
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48582-A/JPW/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-381-0526
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-785-247-13
Query Match 1.2% Score 35.6; DB 3; Length 42;
Best Local Similarity 90.5% Pred. No. 0.099; 4; Indels 0; Gaps 0;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
916 GTCCACATGCTCAGCACACGCTGCTGTGAGCAGCAGATG 957
|||||

Db 1 GTCCACATGTCACACGCTACCGGTGACAGCAGGATG 42

RESULT 2

US-08-785-247-31
Sequence 31, Application US/08785247
Patent No. 6040149

GENERAL INFORMATION:

APPLICANT: Kolesnick, Richard N.
APPLICANT: Liu, Jun
APPLICANT: Zhang, Yuhua
TITLE OF INVENTION: ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
TITLE OF INVENTION: CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
TITLE OF INVENTION: SUPPRESSOR OF RAS, AND METHODS OF USING SAID AGENTS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,247
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48582-A/JPM/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-381-0526

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-785-247-31

Query Match 1.18; Score 32.6; DB 3; Length 39;
Best Local Similarity 89.7%; Pred. No. 0.83;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 919 CACATGTCACACGCTGCTGTGACAGCAGGATG 957
Db 1 CACATGTCACACGCTGCTGTGACAGCAGGATG 39
|||||

RESULT 3

US-08-785-247-14
Sequence 14, Application US/08785247
Patent No. 6040149

GENERAL INFORMATION:

APPLICANT: Kolesnick, Richard N.
APPLICANT: Liu, Jun
APPLICANT: Zhang, Yuhua
TITLE OF INVENTION: ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
TITLE OF INVENTION: CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
TITLE OF INVENTION: SUPPRESSOR OF RAS, AND METHODS OF USING SAID AGENTS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,247
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48582-A/JPM/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-381-0526

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-785-247-14

Query Match 1.18; Score 32.4; DB 3; Length 42;
Best Local Similarity 85.7%; Pred. No. 1;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 916 GTCCACATGTCACACGCTGCTGTGACAGCAGGATG 957
Db 1 GTCCACATGTCACACGCTGCTGTGACAGCAGGATG 42
|||||

RESULT 4

US-08-859-998-979
Sequence 979, Application US/08859998
Patent No. 5994076

GENERAL INFORMATION:

APPLICANT: Chenchik, Alex
APPLICANT: Jorhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 979:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-979

Query Match 0.9%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1704 CAGTTCCAGTCGATGCTACTCTCAT 1731
DB 1 CAGTTCCAGTCGATGCTACTCTCAT 28

RESULT 5
US-09-225-928-979
Sequence 979, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Ridlashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 979:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 979:
US-09-225-928-979

Query Match 0.9%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1704 CAGTTCCAGTCGATGCTACTCTCAT 1731
DB 1 CAGTTCCAGTCGATGCTACTCTCAT 28

RESULT 6
US-08-306-691B-5/c
Sequence 5, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorana & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Nordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-306-691B-5

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATGTGACCGCTCCGCTCCCTCACC 30
DB 26 ATGTGACCGCTCCGCTCCCTCACC 1

RESULT 7
US-08-306-691B-6
Sequence 6, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorana & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-306-691B-6

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATGTACCGCCTCCGCTCCCTCACC 30
|||||
DB 1 ATGTACCGCCTCCGCTCCCTCACC 26

RESULT 8
US-08-859-998-980/C
Sequence 980, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jekhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620

REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 980:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-980

Query Match 0.9%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1963 TCTCTACCGAAGATCAACCGGAGCGC 1988
|||||
DB 26 TCTCTACCGAAGATCAACCGGAGCGC 1

RESULT 9
US-09-225-928-980/C
Sequence 980, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jekhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 980:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 980:
US-09-225-928-980

Query Match 0.9%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1963 TCTCTACCGAATCACCAGCCG 1988
DB 26 TCTCTACCGAATCACCAGCCG 1

RESULT 10

US-08-957-327-2/c
Sequence 2, Application US/08957327
Patent No. 6126965
GENERAL INFORMATION:
APPLICANT: Kasid, Usha
APPLICANT: Gokhale, Prafulla
APPLICANT: Ditschilio, Anatoly
TITLE OF INVENTION: Liposomes containing Oligonucleotides
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,327
FILING DATE: 24-OCT-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Kasid
TELEPHONE: (703) 591-4470
TELEFAX: (703) 591-4428
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-957-327-2

Query Match 0.8%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GCTGCATCATGAGCAGCATACAGG 145
DB 25 GCTGCATCATGAGCAGCATACAGG 1

RESULT 11

US-09-482-084-2/c
Sequence 2, Application US/09482084
Patent No. 6333314
GENERAL INFORMATION:
APPLICANT: Kasid, Usha
APPLICANT: Gokhale, Prafulla
APPLICANT: Ditschilio, Anatoly
APPLICANT: Rahman, Aquilur
TITLE OF INVENTION: Liposomes containing Oligonucleotides

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/482,084
FILING DATE: 13-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,327
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Kasid
TELEPHONE: (703) 591-4470
TELEFAX: (703) 591-4428

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-482-084-2

Query Match 0.8%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GCTGCATCATGAGCAGCATACAGG 145
DB 25 GCTGCATCATGAGCAGCATACAGG 1

RESULT 12

US-08-850-049-17
Sequence 17, Application US/08850049
Patent No. 5965726
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,049

FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-08-850-049-17

Query Match
Best Local Similarity 0.7%; Score 22; DB 2; Length 43;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 2207 TCACAGGCGCTTAACCTCATGTCGCTTCTTCTATC 2244
Db 2 TCTCAGATACCTAGCTTCATATGCTTATGTCTACC 39

RESULT 13
US-08-050-478-17
Sequence 17, Application US/08050478
Patent No. 5972596
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-08-050-478-17

Query Match
Best Local Similarity 0.7%; Score 22; DB 2; Length 43;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 2207 TCACAGGCGCTTAACCTCATGTCGCTTCTTCTATC 2244
Db 2 TCTCAGATACCTAGCTTCATATGCTTATGTCTACC 39

RESULT 14
US-07-858-747B-17
Sequence 17, Application US/07858747B
Patent No. 6174666
GENERAL INFORMATION:
APPLICANT: PAVLAKIS, GEORGE N.; FELBER, BARBARA
APPLICANT: K.
TITLE OF INVENTION: METHOD OF ELIMINATING
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/858,747B
FILING DATE: 19920327
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MARY J. MORRY
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OTHER
HYPOTHETICAL: YES
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: OLIGONUCLEOTIDE FOR MUTATING NT

OTHER INFORMATION: 3392-3434 OF C-FOS, HUMCFOT, ACC #V01512
US-07-858-747B-17

Search completed: May 16, 2003, 12:18:33
Job time: 113 secs

Query Match 0.7%; Score 22; DB 4; Length 43;
Best Local Similarity 73.7%; Pred. No. 1.9e+03;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2207 TCACAGGCGCTTACTGATGTTGCTTCTTCTATC 2244
DB 2 TCTCAGATACCTAGCTTCAATGCTTATGCTTACC 39

RESULT 15

US-09-414-117-17
Sequence 17, Application US/09414117
Patent No. 6291664
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,117
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,049
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-09-414-117-17

Query Match 0.7%; Score 22; DB 4; Length 43;
Best Local Similarity 73.7%; Pred. No. 1.9e+03;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2207 TCACAGGCGCTTACTGATGTTGCTTCTTCTATC 2244
DB 2 TCTCAGATACCTAGCTTCAATGCTTATGCTTACC 39

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 09:19:06 ; Search time 376 Seconds

(without alignments)
10213.154 Million cell updates/sec

Title: US-10-057-550A-64

Perfect score: 2977

Sequence: 1 ccgaatgtgacgcctcccg.....taataaataaataattt 2977

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 810007 seqs, 644969091 residues

Total number of hits satisfying chosen parameters: 482682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications: NA.*
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2: /cgn2_6/ptodata/1/pubpna/PTCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30.6	1.0	31	US-09-801-274-835	Sequence 835, App
2	25	0.8	25	US-09-930-283A-2	Sequence 2, Appl
3	22	0.7	43	US-09-943-722-17	Sequence 17, Appl
4	20.6	0.7	21	US-09-765-081-213	Sequence 213, App
5	20.6	0.7	47	US-09-764-891-10177	Sequence 10177, A
6	20.4	0.7	31	US-09-263-959-580	Sequence 580, App
7	20.4	0.7	41	US-10-085-906-99	Sequence 99, Appl
8	20.2	0.7	46	US-09-827-289-19	Sequence 19, Appl
9	20.2	0.7	46	US-09-827-289-23	Sequence 23, Appl
10	20.2	0.7	48	US-09-822-698A-62	Sequence 62, Appl
11	20	0.7	20	US-10-103-906-4	Sequence 4, Appl
12	20	0.7	20	US-10-078-949-3	Sequence 3, Appl
13	20	0.7	20	US-10-078-949-5	Sequence 5, Appl
14	20	0.7	20	US-10-078-949-7	Sequence 7, Appl
15	20	0.7	20	US-09-835-371-37	Sequence 37, Appl
16	20	0.7	20	US-09-996-263-7	Sequence 7, Appl
17	20	0.7	20	US-09-996-263-8	Sequence 8, Appl
18	20	0.7	20	US-09-996-263-9	Sequence 9, Appl
19	20	0.7	20	US-09-996-263-10	Sequence 10, Appl

C 20	20	0.7	20	9	US-09-996-263-11	Sequence 11, Appl
C 21	20	0.7	20	9	US-09-996-263-12	Sequence 12, Appl
C 22	20	0.7	20	9	US-09-996-263-13	Sequence 13, Appl
C 23	20	0.7	20	9	US-09-996-263-14	Sequence 14, Appl
C 24	20	0.7	20	9	US-09-835-370-37	Sequence 37, Appl
C 25	20	0.7	20	9	US-10-071-822A-1	Sequence 1, Appl
C 26	20	0.7	20	9	US-09-932-300-76	Sequence 76, Appl
C 27	20	0.7	20	9	US-10-057-550-2	Sequence 2, Appl
C 28	20	0.7	20	9	US-10-057-550-3	Sequence 3, Appl
C 29	20	0.7	20	9	US-10-057-550-4	Sequence 4, Appl
C 30	20	0.7	20	9	US-10-057-550-5	Sequence 5, Appl
C 31	20	0.7	20	9	US-10-057-550-6	Sequence 6, Appl
C 32	20	0.7	20	9	US-10-057-550-7	Sequence 7, Appl
C 33	20	0.7	20	9	US-10-057-550-8	Sequence 8, Appl
C 34	20	0.7	20	9	US-10-057-550-9	Sequence 9, Appl
C 35	20	0.7	20	9	US-10-057-550-10	Sequence 10, Appl
C 36	20	0.7	20	9	US-10-057-550-12	Sequence 12, Appl
C 37	20	0.7	20	9	US-10-057-550-13	Sequence 13, Appl
C 38	20	0.7	20	9	US-10-057-550-14	Sequence 14, Appl
C 39	20	0.7	20	9	US-10-057-550-15	Sequence 15, Appl
C 40	20	0.7	20	9	US-10-057-550-16	Sequence 16, Appl
C 41	20	0.7	20	9	US-10-057-550-17	Sequence 17, Appl
C 42	20	0.7	20	9	US-10-057-550-18	Sequence 18, Appl
C 43	20	0.7	20	9	US-10-057-550-19	Sequence 19, Appl
C 44	20	0.7	20	9	US-10-057-550-20	Sequence 20, Appl
C 45	20	0.7	20	9	US-10-057-550-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-801-274-835
Sequence 835, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825, 2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US-60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US-60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 835
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-835
Query Match: 1.0%; Score 30.6; DB 10; Length 31;
Best Local Similarity: 96.8%; Pred. No. 13;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2144 CCCTTTCACAGACGACACACATGTTTC 2174
DB 1 CCCTTTCACAGACGACACACATGTTTC 31
RESULT 2
US-09-930-283A-2/C
Sequence 2, Application US/09930283A
Patent No. US20020160038A1
GENERAL INFORMATION:
APPLICANT: Kasid, Usha
APPLICANT: Gokhale, Prafulla
APPLICANT: Dritschilo, Anatoly
APPLICANT: Rahman, Agulur

TITLE OF INVENTION: Liposomes containing Oligonucleotides
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/930,283A
FILING DATE: 16-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/354,109
FILING DATE: 1999-07-15
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: kasid
TELEPHONE: (703) 591-4470
TELEFAX: (703) 591-4428
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-930-283A-2

Query Match 0.8%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 121 GCTGATCAATGAGACATACAG 145
DB 25 GCTGATCAATGAGACATACAG 1

RESULT 3
US-09-943-722-17
Sequence 17, Application US/09943722
Publication No. US20020192660A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
INHIBITORY/INSTABILITY REGIONS OF MRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/943,722
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,049
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELEPHONE: (212)751-6849
TELEFAX: (212)758-4800
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-09-943-722-17

Query Match 0.7%; Score 22; DB 9; Length 43;
Best Local Similarity 73.7%; Pred. No. 9.3e+03;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 2207 TCACAGGCGCTTAACCTCATGTCCTTTCTATC 2244
DB 2 TCTCAGATACCTGATCTCATGTCCTTTATGCTTAC 39

RESULT 4
US-09-765-081-213
Sequence 213, Application US/09765081
Patent No. US20020037508A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825,2008-001
CURRENT APPLICATION NUMBER: US/09/765,081
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,861
PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 213
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-765-081-213

Query Match 0.7%; Score 20.6; DB 10; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+04;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1237 GGAGATGTTGCACTAAGATC 1257
DB 1 GGAGATGTTGSACTAAGATC 21

Query Match	0.78;	Score 20.4;	DB 10;	Length 31;
Best Local Similarity	95.5%;	Pred. No. 2.4e+04;		
Matches 21; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Query Match	0.7%	Score 20.2;	DB 10;	Length 46;
Best Local Similarity	68.3%;	Pred. No. 3.7e+04;		
Matches 28;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;
OY	2853	TTAATTTGTTTATTCGACCTGCAAAATATCACTATCT	2933	
Db	1	TTTTTTTTTTTTTTAGAGATGCAAAAATCATTTTCAT	41	

RESULT 9
US-09-827-289-23
; Sequence 23, Application US/098226989
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Adarzu, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentl Ver. 2.1
; SEQ ID NO 23
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
US-09-827-289-23

Query Match 0.7%; Score 20.2; DB 10; Length 46;
Best Local Similarity 68.3%; Pred. No. 3.7e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2893 TTAATTGTTTATGACCTGACAAATACAGTTATCT 2933
Db 1 TTTTGTGTTTGTGACGATGACAAATACATTTCTAT 41

RESULT 10
US-09-822-698A-62
; Sequence 62, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: WOClN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 62
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence coding for a mutant CDR3 region
US-09-822-698A-62

Query Match 0.7%; Score 20.2; DB 10; Length 48;
Best Local Similarity 75.8%; Pred. No. 3.8e+04;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 45 GGAGCGGGCGAGAGCTGCCCGCAGACGACAGG 77
Db 13 GGGGGGGCGCAGAGCTGCGACTGACTACTCG 45

RESULT 11
US-10-103-906-4/c
; Sequence 4, Application US/10103906
; Patent No. US20020156268A1
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H.
; APPLICANT: Meilroy, Bethany M.

; TITLE OF INVENTION: Methods for Removing Dimethoxytrityl Groups from
; FILE REFERENCE: ISIS-3349
; CURRENT APPLICATION NUMBER: US/10/103,906
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US/09/271,220
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-103-906-4

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2484 AATGATGACAGCGCGGA 2503
Db 20 AATGATGACAGCGCGGA 1

RESULT 12
US-10-078-949-3
; Sequence 3, Application US/10078949
; Patent No. US20020165189A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Oligonucleotides And Ribonucleases For Cleaving RNA
; FILE REFERENCE: ISIS5027
; CURRENT APPLICATION NUMBER: US/10/078,949
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 08/479,783
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 08/870,608
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/659,440
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentl version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-078-949-3

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.4e+04;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGAATGTGACCGGCTCCG 20
Db 1 CCGAATGTGACCGGCTCCG 20

RESULT 13
US-10-078-949-5
; Sequence 5, Application US/10078949
; Patent No. US20020165189A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; TITLE OF INVENTION: Oligonucleotides And Ribonucleases For Cleaving RNA
; FILE REFERENCE: ISIS5027
; CURRENT APPLICATION NUMBER: US/10/078,949
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/479,783
; PRIOR FILING DATE: 2000-01-07

;; PRIOR APPLICATION NUMBER: 08/870,608
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 08/659,440
;; PRIOR FILING DATE: 1996-06-06
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: Patentln version 3.1
;; SEQ ID NO: 5
;; LENGTH: 20
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oligonucleotide
US-10-078-949-5

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.4e+04;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 127 TCATGAGACATACAGG 146
DB 1 UCAAGGAGACACACAGG 20

RESULT 14
US-10-078-949-7
;; Sequence 7, Application US/10078949
;; Patent No. US20020165189A1
;; GENERAL INFORMATION:
;; APPLICANT: Crooke, Stanley T.
;; TITLE OF INVENTION: Oligoribonucleotides And Ribonucleases For Cleaving RNA
;; FILE REFERENCE: ISIS5027
;; CURRENT APPLICATION NUMBER: US/10/078,949
;; CURRENT FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: 09/479,783
;; PRIOR FILING DATE: 2000-01-07
;; PRIOR APPLICATION NUMBER: 08/870,608
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 08/659,440
;; PRIOR FILING DATE: 1996-06-06
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: Patentln version 3.1
;; SEQ ID NO: 7
;; LENGTH: 20
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Oligonucleotide
US-10-078-949-7

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.4e+04;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2484 AATGATGTACAGCGGGA 2503
DB 1 AAUGCAUGGACAGCGGGA 20

RESULT 15
US-09-835-371-37/C
;; Sequence 37, Application US/09835371
;; Publication No. US20020187473A1
;; GENERAL INFORMATION:
;; APPLICANT: Uhlmann, Eugen
;; APPLICANT: BREIPOHL, Gerhard
;; APPLICANT: WILF, David W
;; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND
;; FILE REFERENCE: 02481.1743 SEQUENCE LISTING
;; CURRENT APPLICATION NUMBER: US/09/835,371
;; CURRENT FILING DATE: 2001-04-17
;; NUMBER OF SEQ ID NOS: 53
;; SOFTWARE: Patentln Ver. 2.1

;; SEQ ID NO: 37
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: base sequence
US-09-835-371-37

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2484 AATGATGTACAGCGGGA 2503
DB 20 AATGATGTACAGCGGGA 1

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Job time: 381 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 06:48:13 ; Search time 6342 Seconds

(without alignments)
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Title: US-10-057-550a-64

Perfect score: 2977
Sequence: 1 ccgaatgacgcctccg.....taataataaataattt 2977

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Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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45:	50	1.7	50	US-10-131-827-3119	Sequence 3119, Ap
46:	50	1.7	50	US-10-131-831-3119	Sequence 3119, Ap
47:	31.6	1.1	48	US-60-253-651-9462	Sequence 9462, Ap
48:	30.6	1.0	31	US-09-801-274-835	Sequence 835, App
49:	30.6	1.0	46	US-60-253-653-25508	Sequence 25508, A
50:	28	0.9	28	US-09-225-201B-979	Sequence 979, App
51:	26	0.9	26	US-08-306-691-5	Sequence 5, Appl1
52:	26	0.9	26	US-08-821-015-5	Sequence 5, Appl1
53:	26	0.9	26	US-08-821-015-5	Sequence 5, Appl1
54:	26	0.9	26	US-09-225-201B-980	Sequence 980, App
55:	25	0.8	25	US-09-354-109-2	Sequence 2, Appl1
56:	25	0.8	25	US-09-396-196F-44994	Sequence 44994, A
57:	25	0.8	25	US-09-396-196F-44995	Sequence 44995, A
58:	25	0.8	25	US-09-396-196F-44996	Sequence 44996, A
59:	25	0.8	25	US-09-396-196F-44997	Sequence 44997, A
60:	25	0.8	25	US-09-396-196F-44998	Sequence 44998, A
61:	25	0.8	25	US-09-396-196F-44999	Sequence 44999, A
62:	25	0.8	25	US-09-396-196F-45000	Sequence 45000, A
63:	25	0.8	25	US-09-396-196F-45001	Sequence 45001, A

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SUMMARIES

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28 25 0.8 25 17 US-09-396-196F-45008 Sequence 45008, A
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35 25 0.8 25 17 US-09-396-196F-45015 Sequence 45015, A
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39 25 0.8 25 17 US-09-396-196F-45019 Sequence 45019, A
40 25 0.8 25 17 US-09-396-196F-45020 Sequence 45020, A
41 25 0.8 25 17 US-09-396-196F-45021 Sequence 45021, A
42 25 0.8 25 17 US-09-396-196F-45022 Sequence 45022, A
43 25 0.8 25 17 US-09-396-196F-45023 Sequence 45023, A
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ALIGNMENTS

RESULT 1

PCT-US01-47856-3119/c

; Sequence 3119, Application PC/TUS0147856

; GENERAL INFORMATION:

; APPLICANT: BIOCARDIA, INC.

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Quetermuth, Thomas

; APPLICANT: Johnson, Frances

; APPLICANT: Fry, Kirk

; APPLICANT: Matcuk, George

; APPLICANT: Prentice, James

; APPLICANT: Phillips, Julie

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Altman, Peter

; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING

; FILE REFERENCE: 506612000140

; CURRENT APPLICATION NUMBER: PCT/US01/47856

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/241,994

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: US 60/296,764

; NUMBER OF SEQ ID NOS: 8832

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3119

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

; PCT-US01-47856-3119

Query Match 1.7%; Score 50; DB 1; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2899 TTGTTTATTCACCTGCACAAATACAGTATCTGATGTCCTCAATT 2948

Db 50 TTGTTTATTCACCTGCACAAATACAGTATCTGATGTCCTCAATT 1

RESULT 2

US-10-131-827-3119/c

; Sequence 3119, Application US/10131827

; GENERAL INFORMATION:

; APPLICANT: BioCardia, Inc.

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Quetermuth, Thomas

; APPLICANT: Johnson, Frances

; APPLICANT: Fry, Kirk

; APPLICANT: Matcuk, George

; APPLICANT: Prentice, James

; APPLICANT: Phillips, Julie

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Altman, Peter

; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING

; FILE REFERENCE: 506612000140

; CURRENT APPLICATION NUMBER: PCT/US01/47856

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/241,994

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: US 60/296,764

; NUMBER OF SEQ ID NOS: 8832

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3119

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

; PCT-US01-47856-3119

Query Match 1.7%; Score 50; DB 1; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2899 TTGTTTATTCACCTGCACAAATACAGTATCTGATGTCCTCAATT 2948

Db 50 TTGTTTATTCACCTGCACAAATACAGTATCTGATGTCCTCAATT 1

RESULT 3

US-10-131-831-3119/c

; Sequence 3119, Application US/10131831

; GENERAL INFORMATION:

; APPLICANT: BioCardia, Inc.

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Quetermuth, Thomas

; APPLICANT: Johnson, Frances

; APPLICANT: Fry, Kirk

; APPLICANT: Matcuk, George

; APPLICANT: Prentice, James

; APPLICANT: Phillips, Julie

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Altman, Peter

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING

; FILE REFERENCE: 506612000121

; CURRENT APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/296,764

; NUMBER OF SEQ ID NOS: 9190

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3119

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-131-831-3119

Query Match 1.7%; Score 50; DB 40; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2899 TTGTTTATTCACCTGCACAAATACAGTATCTGATGTCCTCAATT 2948

Db 50 TTGTTTATTCACCTGCACAAATACAGTATCTGATGTCCTCAATT 1

RESULT 4

US-60-253-651-9462

; Sequence 9462, Application US/60253651

; GENERAL INFORMATION:

; APPLICANT: BioCardia, Inc.

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Quetermuth, Thomas

; APPLICANT: Johnson, Frances

; APPLICANT: Fry, Kirk

; APPLICANT: Matcuk, George

; APPLICANT: Prentice, James

; APPLICANT: Phillips, Julie

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Altman, Peter

; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131,827

; PRIOR FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; PRIOR FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 9090

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3119

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-131-827-3119

Query Match 1.7%; Score 50; DB 40; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2899 TTGTTTATTCACCTGCACAAATACAGTATCTGATGTCCTCAATT 2948

Db 50 TTGTTTATTCACCTGCACAAATACAGTATCTGATGTCCTCAATT 1

;; CURRENT APPLICATION NUMBER: US/60/253,651
;; CURRENT FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 27858
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9462
;; LENGTH: 48
;; TYPE: DNA
;; ORGANISM: Bovine
US-60-253-651-9462

Query Match 1.1%; Score 31.6; DB 69; Length 48;
Best Local Similarity 80.4%; Pred. No. 1.5e+03;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1688 AGGATACCAACCATTCAGTTCGAGTGTCTACTCTATGG 1733
DB 2 AGGACCCGAACCCCTACAGCTTCAGTCTACGCTATGG 47

RESULT 5
US-09-801-274-835
;; Sequence 835, Application US/09801274
;; GENERAL INFORMATION:
;; APPLICANT: Cargill, Michele
;; APPLICANT: Ireland, James S.
;; APPLICANT: Lander, Eric S.
;; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
;; FILE REFERENCE: 2825, 2009-001
;; CURRENT APPLICATION NUMBER: US/09/801,274
;; CURRENT FILING DATE: 2001-03-07
;; PRIOR APPLICATION NUMBER: US 60/187,510
;; PRIOR FILING DATE: 2000-03-07
;; PRIOR APPLICATION NUMBER: US 60/206,129
;; PRIOR FILING DATE: 2000-05-22
;; NUMBER OF SEQ ID NOS: 1802
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 835
;; LENGTH: 31
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-801-274-835

Query Match 1.0%; Score 30.6; DB 31; Length 31;
Best Local Similarity 96.8%; Pred. No. 2.3e+03;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2144 CCCTTCTCAGAGCGAGACACATGTTTC 2174
DB 1 CCCTTCTCAGAGGYAGAACATGTTTC 31

RESULT 6
US-60-253-653-25508
;; Sequence 25508, Application US/60253653
;; GENERAL INFORMATION:
;; APPLICANT: Glenn, Matthew
;; TITLE OF INVENTION: Compositions isolated from ovine tissues
;; FILE REFERENCE: 1057P
;; CURRENT APPLICATION NUMBER: US/60/253,653
;; CURRENT FILING DATE: 2000-11-28
;; NUMBER OF SEQ ID NOS: 30124
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 25508
;; LENGTH: 46
;; TYPE: DNA
;; ORGANISM: Ovine
US-60-253-653-25508

Query Match 1.0%; Score 30.6; DB 69; Length 46;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1184 CCACTCGATTGGTCAGGCTTTTGAACGTATTAGGGA 1228
DB 2 CCACTCCAGTATGATCAGCTCTTCGGGAGCTTTATACGGA 46

RESULT 7
US-09-225-201B-979
;; Sequence 979, Application US/09225201B
;; GENERAL INFORMATION:
;; APPLICANT: Chenchik, Alex
;; APPLICANT: Jorhade, George
;; APPLICANT: Bibilashvili, Robert
;; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;; EXPRESSION
;; NUMBER OF SEQUENCES: 1375
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 2200 Sand Hill Road, Suite 100
;; CITY: Menlo Park
;; STATE: CA
;; COUNTRY: US
;; ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 979:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 979:
US-09-225-201B-979

Query Match 0.9%; Score 28; DB 16; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1704 CAGTTTCAGTGGAGTCTACTCTAT 1731
DB 1 CAGTTTCAGTGGAGTCTACTCTAT 28

RESULT 8
US-08-306-691-5/c
;; Sequence 5, Application US/08306691
;; GENERAL INFORMATION:
;; APPLICANT: Calabretta, Bruno
;; APPLICANT: Skorski, Tomasz
;; TITLE OF INVENTION: ANTISENSE
;; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.

STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-306-691-5

Query Match 0.9%; Score 26; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATGTGACCGCCTCCCGCTCCCTCACC 30
|||||

Db 26 ATGTGACCGCCTCCCGCTCCCTCACC 1

RESULT 9
US-08-306-691-6
Sequence 6, Application US/08306691
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-306-691-6

Query Match 0.9%; Score 26; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATGTGACCGCCTCCCGCTCCCTCACC 30
|||||

Db 1 ATGTGACCGCCTCCCGCTCCCTCACC 26

RESULT 10
US-08-821-015-5/c
Sequence 5, Application US/08821015
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: METHOD FOR INHIBITING NEOPLASTIC CELL
PROLIFERATION WITH ANTISENSE OLIGONUCLEOTIDES TARGETING COO
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,015
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/306,691
FILING DATE: September 15, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8 D11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-821-015-5

Query Match 0.9%; Score 26; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATGTGACCGCCTCCCGCTCCCTCACC 30
|||||

Db 26 ATGTGACCGCCTCCCGCTCCCTCACC 1

RESULT 11
US-08-821-015-6
Sequence 6, Application US/08821015
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: METHOD FOR INHIBITING NEOPLASTIC CELL
TITLE OF INVENTION: PROLIFERATION WITH ANTISENSE OLIGONUCLEOTIDES TARGETING COOPER
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavoigna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,015
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/306,691
FILING DATE: September 15, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8 D11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-821-015-6
Query Match 0.9%; Score 26; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 ATGTGACGGCTCCGCTCCCTCACC 30
Db 1 ATGTGACGGCTCCGCTCCCTCACC 26
RESULT 12
US-09-225-201B-980/C
Sequence 980, Application US/09225201B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bhablashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Fastseq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 980:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-09-225-201B-980
Query Match 0.9%; Score 26; DB 16; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1963 TCTCTACCGAAGATCAACCGAGCGC 1988
Db 26 TCTCTACCGAAGATCAACCGAGCGC 1
RESULT 13
US-09-354-109-2/C
Sequence 2, Application US/09354109
GENERAL INFORMATION:
APPLICANT: Kasid, Usha
APPLICANT: Gokhale, Prafulla
APPLICANT: Dritschilo, Anatoly
APPLICANT: Rahman, Agulur
TITLE OF INVENTION: Liposomes containing Oligonucleotides
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,109
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/957,327
FILING DATE: 24-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Kasid
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 591-4470
TELEFAX: (703) 591-4428
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-09-354-109-2

Query Match 0.8%; Score 25; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 121 GCTGATCATGAGCAGCATACAGG 145
DB 25 GCTGATCATGAGCAGCATACAGG 1

RESULT 14
US-09-396-196F-44994
; Sequence 44994, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44994
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-44994

Query Match 0.8%; Score 25; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1855 AACTGCCCAAGCAATGAGAGGC 1879
DB 1 AACTGCCCAAGCAATGAGAGGC 25

RESULT 15
US-09-396-196F-44995
; Sequence 44995, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44995
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus

US-09-396-196F-44995

Query Match 0.8%; Score 25; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1876 AGGCTGTAGCTGACTGTGTGAGA 1900
DB 1 AGGCTGTAGCTGACTGTGTGAGA 25

Search completed: May 16, 2003, 12:16:27
Job time : 6348 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 07:11:11 ; Search time 1366 Seconds

11277.539 Million cell updates/sec

Title: US-10-057-550A-64
Perforated paper: 2077

Sequence: 1 ccgaatgtgaccgcctccg.....taataaataaataat 2977

Gapop 10.0 , Gapext 1.0

Searched: 6404235 seqs, 2587356060 residues

Total number of hits satisfying chosen parameters: 7758442

Maximum DB seq length: 50

Post-processing: Minimum Match 08

Listing first 45 summaries

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Database : Pending_Patents_NA_New:*
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- 1: /cgn2_6/pdatata/2/pna/PCF_NEW_COMB_seg.*
- 2: /cgn2_6/pdatata/2/pna/U506_NEW_COMB_seg.*
- 3: /cgn2_6/pdatata/2/pna/U507_NEW_COMB_seg.*
- 4: /cgn2_6/pdatata/2/pna/U508_NEW_COMB_seg.*
- 5: /cgn2_6/pdatata/2/pna/U509_NEW_COMB_seg.*
- 6: /cgn2_6/pdatata/2/pna/U509_NEW_COMB_seg2.*
- 7: /cgn2_6/pdatata/2/pna/U509_NEW_COMB_seg3.*
- 8: /cgn2_6/pdatata/2/pna/U510_NEW_COMB_seg.*
- 9: /cgn2_6/pdatata/2/pna/U510_NEW_COMB_seg2.*
- 10: /cgn2_6/pdatata/2/pna/U560_NEW_COMB_seg.*
- 11: /cgn2_6/pdatata/2/pna/U560_NEW_COMB_seg2.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	50	1.7	50	9	US-10-325-899-3119	Sequence 3119, AP
C 2	25	0.8	25	11	US-10-075-994/-2	Sequence 2, AP11
C 3	23.4	0.8	25	11	US-60-427-808-320641	Sequence 320641, AP
C 4	23.4	0.8	25	11	US-60-427-808-55623	Sequence 55623, AP
C 5	23.4	0.8	25	11	US-60-427-808-917222	Sequence 917222, AP
C 6	23.4	0.8	25	11	US-60-427-835-397923	Sequence 397923, AP
C 7	23	0.8	50	9	US-10-325-899-5803	Sequence 5803, AP
C 8	22.4	0.8	43	11	US-60-434-832-1070	Sequence 1070, AP
C 9	22.4	0.7	45	11	US-60-288-292-19321	Sequence 19321, AP
C 10	22	0.7	22	9	US-10-293-338-4068	Sequence 4068, AP
C 11	22	0.7	47	9	US-10-349-143-3876	Sequence 3876, AP
C 12	21.8	0.7	25	1	PCT-US03-14877A-875	Sequence 875, AP
C 13	21.8	0.7	25	11	US-60-427-808-330640	Sequence 330640, AP
C 14	21.8	0.7	25	11	US-60-427-808-55622	Sequence 55622, AP
C 15	21.8	0.7	25	11	US-60-427-808-917221	Sequence 917221, AP
C 16	21.8	0.7	25	11	US-60-427-835-397922	Sequence 397922, AP
C 17	21.8	0.7	39	8	US-10-287-787-18691	Sequence 18691, AP
C 18	21.8	0.7	39	8	US-10-287-787-18692	Sequence 18692, AP
C 19	21.8	0.7	39	8	US-10-287-787-18693	Sequence 18693, AP
C 20	21.8	0.7	50	6	US-10-287-787-19984	Sequence 19984, AP
C 21	21.6	0.7	50	6	US-09-912-293-210904	Sequence 210904, AP
C 22	21.6	0.7	50	9	US-10-325-899-47714	Sequence 47714, AP

C 23	23	-21.4	0.7	25	11	US-60-427-808-116035	Sequence 116035,
C 24	24	-21.4	0.7	55	6	US-09-912-293-130705	Sequence 130705,
C 25	25	-21.2	0.7	45	8	US-10-287-787-4937	Sequence 4937, AP
C 26	26	-21.2	0.7	47	8	US-10-287-787-4936	Sequence 4936, AP
C 27	27	-21.2	0.7	49	8	US-10-389-048-4355	Sequence 4355, AP
C 28	28	-21	0.7	44	8	US-10-287-787-19789	Sequence 19789, AP
C 29	29	-21	0.7	44	8	US-10-287-787-19790	Sequence 19790, AP
C 30	30	-21	0.7	47	9	US-10-349-143-2948	Sequence 2948, AP
C 31	31	-21	0.7	50	6	US-09-912-293-242736	Sequence 242736, AP
C 32	32	-21	0.7	50	9	US-10-325-899-3101	Sequence 3101, AP
C 33	33	-21	0.7	50	9	US-10-325-899-8045	Sequence 8045, AP
C 34	34	-20.8	0.7	25	11	US-60-427-808-630641	Sequence 50641, AP
C 35	35	-20.8	0.7	25	11	US-60-427-808-630023	Sequence 630023, AP
C 36	36	-20.8	0.7	25	11	US-60-427-808-943561	Sequence 943561, AP
C 37	37	-20.8	0.7	25	11	US-60-427-836-451365	Sequence 451365, AP
C 38	38	-20.8	0.7	25	9	US-10-325-899-7636	Sequence 7636, AP
C 39	39	-20.6	0.7	45	8	US-10-287-787-19197	Sequence 19197, AP
C 40	40	-20.6	0.7	50	6	US-09-912-293-43884	Sequence 43884, AP
C 41	41	-20.6	0.7	45	8	US-10-325-899-1696	Sequence 1696, AP
C 42	42	-20.4	0.7	45	8	US-10-287-787-21968	Sequence 21968, AP
C 43	43	-20.4	0.7	45	8	US-10-287-787-21970	Sequence 21970, AP
C 44	44	-20.4	0.7	50	9	US-10-325-899-3367	Sequence 3367, AP
C 45	45	-20.4	0.7	50	9	US-10-325-899-4603	Sequence 4603, AP

ALIGNMENTS

```

RESULT 1
US-10-325-899-3119/c
; Sequence 3119, Application US/10325899
GENERAL INFORMATION:
APPLICANT: Wollgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPL
TITLE OF INVENTION: REJECTION
FILE REFERENCE: 506612000122
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3119
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-899-3119

Query Match      1.7%; Score 50; DB %; Length 50;
Best Local Similarity 100.0%; Pred. No. 0 00061;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2899 TTGTTTTATTGCACCTGACAAAATACAGTTATCTGATGTCCCTCAATT 2948
|||||
|||
bb 50 TTGTTTTATTGCACCTGACAAAATACAGTTATCTGATGTCCCTCAATT 1

RESULT 2
US-10-075-994A-2/c
; Sequence 2, Application US/10075994A
GENERAL INFORMATION:
APPLICANT: KASID, Usha
APPLICANT: GOKHALE, Pratulla
APPLICANT: PIR, Jin
APPLICANT: MENANI, Rajshree
APPLICANT: AHMAD, Imran

```

APPLICANT: DRITSCHILLO, Anatoly
APPLICANT: RAHMAN, Aquilur
TITLE OF INVENTION: CHEMOSENSITIZING WITH LIPOSOMES CONTAINING OLIGONUCLEOTIDES
FILE REFERENCE: 219604
CURRENT APPLICATION NUMBER: US/10/075,994A
CURRENT FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-075-994A-2

Query Match
Best Local Similarity 0.8%; Score 25; DB 8; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 121 GCTGATCAATGAGCAGCATACAG 145
DB 25 GCTGATCAATGAGCAGCATACAG 1

RESULT 3
US-60-427-808-320641
Sequence 320641, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 320641
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-60-427-808-320641

Query Match
Best Local Similarity 0.8%; Score 23.4; DB 11; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2210 CAGGCGCTTACTTCATTCCTT 2234
DB 1 CAGGCGCTTACTTCATTCCTT 25

RESULT 4
US-60-427-808-556623
Sequence 556623, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 556623
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-60-427-808-556623

Query Match
Best Local Similarity 0.8%; Score 23.4; DB 11; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2214 GCCTTACTTCATTCGCTTCTTT 2238

DB 1 GCCTTACTTCATTCGCTTCTTT 25

RESULT 5
US-60-427-808-917222
Sequence 917222, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 917222
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-60-427-808-917222

Query Match
Best Local Similarity 0.8%; Score 23.4; DB 11; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2217 TTAAGTCATGTTGCTTCTTTCT 2241
DB 1 TTAAGTCATGTTGCTTCTTTCT 25

RESULT 6
US-60-427-836-397923
Sequence 397923, Application US/60427836
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527
CURRENT APPLICATION NUMBER: US/60/427,836
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 397923
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-60-427-836-397923

Query Match
Best Local Similarity 0.8%; Score 23.4; DB 11; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2214 GCCTTACTTCATTCGCTTCTTT 2238
DB 1 GCCTTACTTCATTCGCTTCTTT 25

RESULT 7
US-10-325-899-5803/c
Sequence 5803, Application US/10325899
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPL
FILE REFERENCE: 506612000122
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22

RESULT 12
PCT-US02-14877A-875
; Sequence 875, Application PC/TUS0214877A
; GENERAL INFORMATION:

```

; APPLICANT: Genome Therapeutics Corporation and
; APPLICANT: Allen, Kristina M.
; APPLICANT: Yaworsky, Paul
; APPLICANT: Morales, Arturo J.
; APPLICANT: Graham, James R.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
; FILE REFERENCE: 032796-135
; CURRENT APPLICATION NUMBER: PCT/US02/14877A
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; PCT-US02-14877A-875

```

Query Match

```

Best Local Similarity 0.7%; Score 21.8; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2796 TCTCTACAAACAACAACAACA 2820

```

```

Db 1 TCTCAACAACAACAACAACAACA 25

```

RESULT 13

```

; US-60-427-808-320640
; Sequence 320640, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 320640
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-60-427-808-320640

```

Query Match

```

Best Local Similarity 0.7%; Score 21.8; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2210 CAGGGCCTTAATTCATGTCCTT 2234

```

```

Db 1 CAGGGCCTTAATTCATGTCCTT 25

```

RESULT 14

```

; US-60-427-808-556622
; Sequence 556622, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20

```

```

; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 556622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-60-427-808-556622

```

Query Match

```

Best Local Similarity 0.7%; Score 21.8; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2214 GCCTTAATTCATGTCCTTCTT 2238

```

```

Db 1 GCCTTAATTCATGTCCTTCTT 25

```

RESULT 15

```

; US-60-427-808-917221
; Sequence 917221, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 917221
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-60-427-808-917221

```

Query Match

```

Best Local Similarity 0.7%; Score 21.8; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2217 TTAATTCATGTCCTTCTTCTT 2241

```

```

Db 1 TTAATTCATGTCCTTCTTCTT 25

```

```

Search completed: May 16, 2003, 12:41:39
Job time : 1374 secs

```

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 05:51:03 ; Search time 4039 Seconds
(without alignments)
11937.104 Million cell updates/sec

Title: US-10-057-550A-64

Perfect score: 2977

Sequence: 1 ccgaatgaccgcctcccg.....taataaataaataaattt 2977

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estp1:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gd_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.8	1.4	48	14	H26959
2	24.6	0.8	47	17	AZ425831
3	22.8	0.8	45	2	HSW002199
4	22	0.7	40	17	AZ391073
5	22	0.7	43	12	BB969098
6	21.8	0.7	47	13	BJ047667

C	7	21.8	0.7	49	9	A1316598
C	8	21.6	0.7	49	17	AZ593107
C	9	21.6	0.7	45	2	HSW003616
C	10	21.4	0.7	50	9	AU270282
C	11	21	0.7	43	17	AZ310534
C	12	21	0.7	44	9	AL587842
C	13	20.8	0.7	36	17	AZ512567
C	14	20.8	0.7	44	2	HSW001110
C	15	20.8	0.7	45	17	AZ602556
C	16	20.8	0.7	49	9	A1267816
C	17	20.8	0.7	50	9	AU102743
C	18	20.8	0.7	50	12	BF013308
C	19	20.6	0.7	46	9	AA737998
C	20	20.6	0.7	46	9	A1360975
C	21	20.6	0.7	50	9	A1708455
C	22	20.4	0.7	36	17	AZ774766
C	23	20.4	0.7	40	9	AL048749
C	24	20.4	0.7	46	9	A1439612
C	25	20.4	0.7	48	17	DR15019T
C	26	20.4	0.7	49	9	A1173140
C	27	20.4	0.7	50	9	AU104895
C	28	20.4	0.7	50	17	AZ347604
C	29	20.2	0.7	36	14	TS7700
C	30	20.2	0.7	49	17	AZ803783
C	31	20.2	0.7	50	9	AA139046
C	32	20.2	0.7	37	10	BQ258029
C	33	20	0.7	37	10	AA334659
C	34	20	0.7	39	13	BJ065085
C	35	20	0.7	39	17	BJ96875
C	36	20	0.7	40	17	BJ96875
C	37	20	0.7	41	17	AZ793496
C	38	20	0.7	43	9	A1608816
C	39	20	0.7	46	17	AZ806877
C	40	20	0.7	49	9	AA388129
C	41	20	0.7	50	9	AA853120
C	42	20	0.7	50	9	AJ499559
C	43	20	0.7	50	9	AU104458
C	44	20	0.7	50	9	AU104922
C	45	20	0.7	50	9	AA564185
C	45	20	0.7	50	13	BI496942

ALIGNMENTS

RESULT 1	H26959	LOCUS	H26959	DEFINITION	H26959	48 bp	mRNA	linear	EST 16-AUG-1995
ACCESSION	Y058C08.s1	VERSION	IMAGE:182126.3	KEYWORDS	SERINE/THROMBIN-PROTEIN KINASE (HUMAN); mRNA sequence.				
ORIGIN	H26959.1	ORGANISM	human	REFERENCE	1 (bases 1 to 48)				
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.								
TITLE	The WashU-Werk EST Project								
JOURNAL	Unpublished (1995)								
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu Insert Size: 603 High quality sequence starts: 1 High quality sequence stops: 1								

ant, F-"
rom M

FEATURES

High quality sequence stop: 47.
Location/qualifiers

CC	Berlin-Charlottenburg, GERMANY; Email: clone@czpd.de	.	.
XX		.	.
HH	Key	.	.
	Location/Qualifiers	.	.

10-5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1(4732)114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptor and purified. The sheared, adapted mouse DNA was annealed to adaptered vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

```
BASE COUNT      0 a          0 c          8 g         32 t
ORIGIN
Query Match     0.7% Score 22; DB 17; Length 40;
Best Local Similarity 73.7%; Pred. No. 8.6e+05;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

DQ 2872 GTTTCTTGATGATTGGGTAAATTTTTTGAATTAAT 2909
||||| |||| | |||| ||||| ||||| ||
Ddb 1 GTTTGTTTGTTCGTTTCGTTTCGTTTCGTTTCGTTTCGTT TC 38

```
RESULT 5       BE969098             43 bp mRNA linear EST_04-Oct-2000
LOCUS        BE969098
DEFINITION   601650077R1 NIH_MGC_74 Homo sapiens cdna clone IMAGE:3933811 3',
ACCESSION    BE969098
VERSION      BE969098
KEYWORDS     NIH-MGC http://mgc.ncl.nih.gov/.
SOURCE       EST.
ORGANISM     human.
REFERENCE    1 (bases 1 to 43)
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE        Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC Clone Distribution Information can be  
found through the I.M.A.G.E. Consortium/LNML at:  
http://image.llnl.gov  
Plate: LNCMT73 row: j column: 20.
```

```
FEATURES
Source
1..43
 /organism="Homo sapiens"  
 /db_xref="taxon:9606"  
 /clone_image="IMAGE:3933811"  
 /clone_id="NIH_MGC_74"  
 /lab_host="DH10B (TI phage-resistant)"  
 /note="Organ: heart; Vector: pDR-LIB (Clontech); Site_1:  
 : SflI (ggcgccgtgcgc); Site_2: SflI (ggccattatgcc); 5'  
 and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-CACGCCCATTTAAGCC-3' and 3' adaptor  
 sequence: 5'-ATTCGTAGAAGCGCAGCGCCGCAATG-dt(30)BN-3'  
 (where B = A, C, or G and N = A, C, G, or T). Average  
 insert size 1.25 kb (range 0.6-4.0 kb). 14/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 laboratories (Palo Alto, CA)."
BASE COUNT      0 a          1 c          4 g         38 t
ORIGIN
```

```
Query Match     0.7% Score 22; DB 12; Length 43;  
Best Local Similarity 73.7%; Pred. No. 8.7e+05;  
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

DY 2872 GTTTCCTTGATGATTGGGTAAATTTTATTTAT 2909
||||| |||| | |||| ||||| ||||| ||

FEATURES	source	Location/Qualifiers
Seq primer: -40RP from Glbco.	1..49	
	/organism="Mus musculus"	
	/db_xref="taxon:10090"	
	/clone="IMAGE:1973550"	
	/clone_lib="Schiller mouse MAC16"	
	/cell_line="colon cancer cell line"	
	/lab_host="SOLR"	
	/note="Vector: pBluescript SK- (Stratagene); Site 1: EcoRI ; Site 2: XhoI; double-stranded cDNA was prepared from cell line MAC16 using primer	
	5'-GAGAGACAGACAGACAGACAGACAGACTGCTGCT(18)-3'. An EcoRI adaptor was used on the 5' end of the cDNA as follows: 5'-AATTCGACAGACAG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."	

BASE COUNT	40 a	4 c	4 g	1 t
ORIGIN				
Query Match	0.7%;	Score 21.8;	DB 9;	Length 49;
Best Local Similarity	65.3%;	Pred. No. 1e+06;		
Matches 32;	Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0;

Db	49 G	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGCTGCCGA 1
0Y	2872	CTTTCTTGATGATTTGGGTTTAAATTTGTTTATTCACACTGACAA 2920
LOCUS	AZ593107/c	49 bp DNA linear GSS 13-DEC-2000
DEFINITION	IM0404022F Mouse 10kb plasmid U06C1M library Mus musculus genomic	
ACCESSION	AZ593107	
VERSION	AZ593107.1	GI:11715297
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 49)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	
TITLE	Mus whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0404 row: 0 column: 22 Seq primer: CTTGTAAACGACGCCACT	

ACCESSION clone UUGC1M0025J03 R, DNA sequence.
VERSION A2310534
KEYWORDS A2310534.1 GI:10352617
SOURCE GSS.
ORGANISM house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 43)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: J column: 03
Seq primer: CACACAGCAACAGCTAGACC
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
1..43
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0025J03"
/clone_lib="Mouse 10kb plasmid library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473211419b1a129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 26 a 10 c 4 g 3 t
ORIGIN

Query Match 0.7%; Score 21; DB 17; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 AACAAACAACAACAACAG 2821
|||||
Db 5 AACAAACAACAACAACAG 25

RESULT 12
AL587842 44 bp mRNA linear EST 02-MAR-2001
LOCUS
DEFINITION AL587842 BP Chicken Brain Library Gallus gallus cDNA clone

ACCESSION ROS064C05, mRNA sequence.
VERSION AL587842
KEYWORDS AL587842.1 GI:13192876
SOURCE EST.
ORGANISM chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
REFERENCE 1 (bases 1 to 44)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bdsr.ac.uk
GCAGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-1)
Seq primer: M13F.
Location/Qualifiers
1..44
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS064C05"
/clone_lib="BP Chicken Brain Library"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/note="Vector: pSPOR1; Site.1: NotI; Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TGACCTGAG 3'; 3' adaptor sequence: 5' GCAGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-1)"
Clonetecc (*6854-1)"

BASE COUNT 1 a 0 c 4 g 39 t
ORIGIN

Query Match 0.7%; Score 21; DB 9; Length 44;
Best Local Similarity 73.0%; Pred. No. 1.6e+06;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2873 TTTCTTGATGATTTGGCTTTAATTTGTTTATTT 2909
|||||
Db 4 TTTTCTTTTCTTTTGGCTTTTCTTTTCTTTT 40

RESULT 13
A2512567/c 36 bp DNA linear GSS 05-OCT-2000
LOCUS
DEFINITION IM0356G1F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0356G1 F, DNA sequence.
ACCESSION A2512567
VERSION A2512567.1 GI:10693883
KEYWORDS GSS.
SOURCE house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 36)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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/note-Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 1 a 4 c 8 g 32 t
ORIGIN

Query Match

Best Local Similarity 91.7%; Score 20.8; DB 17; Length 45;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2799 CTACCAAAACAACAACACACG 2822

Db 39 CAAACAAACAACAACAACAACAC 16

Search completed: May 16, 2003, 10:26:05
Job time : 4055 secs